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Sequence Listing was accepted.

If you need help call the Patent Electronic Business Center at (866)
217-9197 (toll free).

Reviewer: Durreshwar Anjum

Timestamp: [year=2011; month=10; day=6; hr=14; min=47; sec=18; ms=814;]

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Application No: 10594189 Version No: 1.0

Input Set:

Output Set:

Started: 2011-09-29 15:43:17.530
Finished: 2011-09-29 15:43:21.703
Elapsed: 0 hr(s) 0 min(s) 4 sec(s) 173 ms
Total Warnings: 41
Total Errors: 0
No. of SeqIDs Defined: 41
Actual SeqID Count: 41

Error code	Error Description
W 402	Undefined organism found in <213> in SEQ ID (1)
W 213	Artificial or Unknown found in <213> in SEQ ID (2)
W 213	Artificial or Unknown found in <213> in SEQ ID (3)
W 213	Artificial or Unknown found in <213> in SEQ ID (4)
W 213	Artificial or Unknown found in <213> in SEQ ID (5)
W 213	Artificial or Unknown found in <213> in SEQ ID (6)
W 213	Artificial or Unknown found in <213> in SEQ ID (7)
W 213	Artificial or Unknown found in <213> in SEQ ID (8)
W 213	Artificial or Unknown found in <213> in SEQ ID (9)
W 213	Artificial or Unknown found in <213> in SEQ ID (10)
W 213	Artificial or Unknown found in <213> in SEQ ID (11)
W 213	Artificial or Unknown found in <213> in SEQ ID (12)
W 213	Artificial or Unknown found in <213> in SEQ ID (13)
W 213	Artificial or Unknown found in <213> in SEQ ID (14)
W 213	Artificial or Unknown found in <213> in SEQ ID (15)
W 213	Artificial or Unknown found in <213> in SEQ ID (16)
W 213	Artificial or Unknown found in <213> in SEQ ID (17)
W 213	Artificial or Unknown found in <213> in SEQ ID (18)
W 213	Artificial or Unknown found in <213> in SEQ ID (19)
W 213	Artificial or Unknown found in <213> in SEQ ID (20)

Input Set:

Output Set:

Started: 2011-09-29 15:43:17.530
Finished: 2011-09-29 15:43:21.703
Elapsed: 0 hr(s) 0 min(s) 4 sec(s) 173 ms
Total Warnings: 41
Total Errors: 0
No. of SeqIDs Defined: 41
Actual SeqID Count: 41

Error code	Error Description
W 213	Artificial or Unknown found in <213> in SEQ ID (21) This error has occurred more than 20 times, will not be displayed

SEQUENCE LISTING

<110> Universitaet Stuttgart
 PFIZENMAIER, Klaus
 SCHEURICH, Peter
 GRUNWALD, Ingo
 KRIPPNER-HEIDENREICH, Anja

<120> RECOMBINANT POLYPEPTIDES OF THE MEMBERS OF THE TNF LIGAND FAMILY AND USE THEREOF

<130> 040045-0358701

<140> 10594189

<141> 2011-09-29

<150> PCT/EP2005/003158

<151> 2005-03-24

<150> DE 102004014983.6-4

<151> 2004-03-26

<160> 41

<170> PatentIn version 3.3

<210> 1

<211> 8

<212> PRT

<213> Artificial Sequence Sequence

<220>

<223> Description of Artificial Sequence: Synthetic flag-tag peptide sequence

<400> 1

Asp Tyr Lys Asp Asp Asp Asp Lys
 1 5

<210> 2

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Peptide linker sequence

<400> 2

Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser
 1 5 10

<210> 3

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Peptide linker sequence

<400> 3

Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser
1 5 10 15

<210> 4

<211> 36

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Linker sequence

<400> 4

ggtggcggtt ctggtggcgg ttctggtggc ggatcc 36

<210> 5

<211> 48

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Linker sequence

<400> 5

ggtggcggtt ctggtggcgg ttctggtggc ggttctggtg gcggatcc 48

<210> 6

<211> 84

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: scTNF Primer I

<400> 6

tcgattaagc ttcccggggg atccgccacc agaaccgccca ccagaaccgc caccagagc 60

gatgataccg aagtaaacct gacc 84

<210> 7

<211> 97

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: scTNF Primer II

<400> 7
 atcgattaag cttcccgggg gatccgccac cagaaccgcc accagaaccg ccaccagaac 60
 cgccaccag agcgatgata ccgaagtaaa cctgacc 97

<210> 8
 <211> 43
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: scTNF Primer III

<400> 8
 cccgaattc ggatcctctt ctcgtacccc gtctgacaaa ccg 43

<210> 9
 <211> 53
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: scTNF Primer IV

<400> 9
 gggggggaag cttatcgata gttagatatc atcacagagc gatgataccg aag 53

<210> 10
 <211> 41
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: scTNF Primer V

<400> 10
 cctgtacctg atctactccc aggttctgtt caaaggccag g 41

<210> 11
 <211> 97
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: cys-scTNF Primer VI

<400> 11
 aattcattaa agaggagaaa ttaactatgg gagagctcat cgaaggtcgc tgcgccggtg 60
 gatctgggtca tcatcatcac catcacggct cagacgg 97

<210> 12

<211> 97
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: cys-scTNF Primer VII

 <400> 12
 cgctccgtct gagccgtgat ggtgatgatg atgaccagat ccaccggcgc agcgaccttc 60

 gatgagctct cccatagtta atttctcttc tttaatg 97

 <210> 13
 <211> 100
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Primer FasL#1R

 <400> 13
 atcgatttct agaccgggg gatccgccac cagaaccgcc accagaaccg ccaccagaac 60

 cgccaccgag cttatataag ccgaaaaacg tctgagattc 100

 <210> 14
 <211> 35
 <212> DNA
 <213> Artificial Sequence

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 <223> Description of Artificial Sequence: Primer FasL#2F

 <400> 14
 ggggtagcgg ccgcgctgtc gacgattaca aagac 35

 <210> 15
 <211> 26
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Primer FasL#3F

 <400> 15
 agaaaaaaag gagctgagga aagtgg 26

 <210> 16
 <211> 36
 <212> DNA
 <213> Artificial Sequence

 <220>

<223> Description of Artificial Sequence: Primer FasL#4F

<400> 16
ggggcgatc cgaaaaaag gagctgagga aagtgg 36

<210> 17
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer FasL#5R

<400> 17
ggggcctcta gaatcgatgg tcagagctta tataagccga aaaacgtctg 50

<210> 18
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer HA-IF

<400> 18
cgccatggct atcatctacc tcatactcct gttcacgct gtgcggggag c 51

<210> 19
<211> 60
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer HA-IIR

<400> 19
ggccgctgcc ccgcacagcg gtgaacagga ggatgaggta gatgatagcc atggcggtac 60

<210> 20
<211> 106
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer TRAIL#1R

<400> 20
atcgatttct agaccgggg gatccgccac cagaaccgcc accagaaccg ccaccagaac 60

cgccaccgcc aactaaaaag gccccgaaaa aactggcttc atggtc 106

<210> 21

<211> 46
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Primer TRAIL#2F

 <400> 21
 ggggtagaat tcggaacctc tgaggaaacc atttctacag ttcaag 46

 <210> 22
 <211> 26
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Primer TRAIL#3F

 <400> 22
 aacctctgag gaaaccattt ctacag 26

 <210> 23
 <211> 36
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Primer TRAIL#4F

 <400> 23
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 <210> 24
 <211> 53
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Primer TRAIL#5R

 <400> 24
 ggggcctcta gaatcgatgg tcagccaact aaaaaggccc cgaaaaaact ggc 53

 <210> 25
 <211> 1506
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: scTNF-L short chain

 <220>

<221> CDS

<222> (1)..(1503)

<400> 25

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Met	Arg	Gly	Ser	His	His	His	His	His	His	Gly	Ser	Ala	Ser	Ser	Ser	
1				5						10					15	

tct	cgt	acc	ccg	tct	gac	aaa	ccg	gtt	gct	cac	gtt	gtt	gca	aac	ccg	96
Ser	Arg	Thr	Pro	Ser	Asp	Lys	Pro	Val	Ala	His	Val	Val	Ala	Asn	Pro	
			20					25					30			

cag	gct	gaa	ggg	caa	ctg	caa	tgg	ctg	aac	cgt	cgt	gct	aac	gct	ctg	144
Gln	Ala	Glu	Gly	Gln	Leu	Gln	Trp	Leu	Asn	Arg	Arg	Ala	Asn	Ala	Leu	
		35					40					45				

ctg	gct	aac	ggg	gtt	gaa	ctg	cgt	gac	aac	cag	ctg	gtt	gtt	ccg	tct	192
Leu	Ala	Asn	Gly	Val	Glu	Leu	Arg	Asp	Asn	Gln	Leu	Val	Val	Pro	Ser	
	50					55					60					

gaa	ggc	ctg	tac	ctg	atc	tac	tcc	cag	gtt	ctg	ttc	aaa	ggc	cag	ggc	240
Glu	Gly	Leu	Tyr	Leu	Ile	Tyr	Ser	Gln	Val	Leu	Phe	Lys	Gly	Gln	Gly	
65					70					75					80	

tgc	ccg	tcc	acc	cac	gtt	ctg	ctg	acc	cac	acc	atc	tct	cgt	atc	gct	288
Cys	Pro	Ser	Thr	His	Val	Leu	Leu	Thr	His	Thr	Ile	Ser	Arg	Ile	Ala	
				85					90					95		

gtt	tcc	tac	cag	acc	aaa	gta	aac	ctg	ctg	tct	gca	atc	aaa	tct	ccg	336
Val	Ser	Tyr	Gln	Thr	Lys	Val	Asn	Leu	Leu	Ser	Ala	Ile	Lys	Ser	Pro	
			100					105					110			

tgc	cag	cgt	gaa	acc	ccg	gaa	ggg	gct	gaa	gct	aaa	ccg	tgg	tac	gaa	384
Cys	Gln	Arg	Glu	Thr	Pro	Glu	Gly	Ala	Glu	Ala	Lys	Pro	Trp	Tyr	Glu	
		115					120					125				

ccg	atc	tac	ctg	ggg	ggc	gtt	ttt	caa	ctg	gag	aaa	ggg	gac	cgt	ctg	432
Pro	Ile	Tyr	Leu	Gly	Gly	Val	Phe	Gln	Leu	Glu	Lys	Gly	Asp	Arg	Leu	
	130					135					140					

tct	gca	gaa	att	aac	cgt	ccg	gac	tac	ctg	gac	ttc	gca	gaa	tct	ggg	480
Ser	Ala	Glu	Ile	Asn	Arg	Pro	Asp	Tyr	Leu	Asp	Phe	Ala	Glu	Ser	Gly	
145				150					155					160		

cag	gtt	tac	ttc	ggg	atc	atc	gct	ctg	ggg	ggc	ggg	tct	ggg	ggc	ggg	528
Gln	Val	Tyr	Phe	Gly	Ile	Ile	Ala	Leu	Gly	Gly	Gly	Ser	Gly	Gly	Gly	
			165					170					175			

tct	ggg	ggc	gga	tcc	tct	tct	cgt	acc	ccg	tct	gac	aaa	ccg	gtt	gct	576
Ser	Gly	Gly	Gly	Ser	Ser	Ser	Arg	Thr	Pro	Ser	Asp	Lys	Pro	Val	Ala	
			180					185					190			

cac	gtt	gtt	gca	aac	ccg	cag	gct	gaa	ggg	caa	ctg	caa	tgg	ctg	aac	624
His	Val	Val	Ala	Asn	Pro	Gln	Ala	Glu	Gly	Gln	Leu	Gln	Trp	Leu	Asn	
			195				200					205				

cgt	cgt	gct	aac	gct	ctg	ctg	gct	aac	ggg	gtt	gaa	ctg	cgt	gac	aac	672
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Arg Arg Ala Asn Ala Leu Leu Ala Asn Gly Val Glu Leu Arg Asp Asn	
210 215 220	
cag ctg gtt gtt ccg tct gaa ggc ctg tac ctg atc tac tcc cag gtt	720
Gln Leu Val Val Pro Ser Glu Gly Leu Tyr Leu Ile Tyr Ser Gln Val	
225 230 235 240	
ctg ttc aaa ggc cag ggc tgc ccg tcc acc cac gtt ctg ctg acc cac	768
Leu Phe Lys Gly Gln Gly Cys Pro Ser Thr His Val Leu Leu Thr His	
245 250 255	
acc atc tct cgt atc gct gtt tcc tac cag acc aaa gta aac ctg ctg	816
Thr Ile Ser Arg Ile Ala Val Ser Tyr Gln Thr Lys Val Asn Leu Leu	
260 265 270	
tct gca atc aaa tct ccg tgc cag cgt gaa acc ccg gaa ggt gct gaa	864
Ser Ala Ile Lys Ser Pro Cys Gln Arg Glu Thr Pro Glu Gly Ala Glu	
275 280 285	
gct aaa ccg tgg tac gaa ccg atc tac ctg ggt ggc gtt ttt caa ctg	912
Ala Lys Pro Trp Tyr Glu Pro Ile Tyr Leu Gly Gly Val Phe Gln Leu	
290 295 300	
gag aaa ggt gac cgt ctg tct gca gaa att aac cgt ccg gac tac ctg	960
Glu Lys Gly Asp Arg Leu Ser Ala Glu Ile Asn Arg Pro Asp Tyr Leu	
305 310 315 320	
gac ttc gca gaa tct ggt cag gtt tac ttc ggt atc atc gct ctg ggt	1008
Asp Phe Ala Glu Ser Gly Gln Val Tyr Phe Gly Ile Ile Ala Leu Gly	
325 330 335	
ggc ggt tct ggt ggc ggt tct ggt ggc gga tcc tct tct cgt acc ccg	1056
Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Ser Ser Arg Thr Pro	
340 345 350	
tct gac aaa ccg gtt gct cac gtt gtt gca aac ccg cag gct gaa ggt	1104
Ser Asp Lys Pro Val Ala His Val Val Ala Asn Pro Gln Ala Glu Gly	
355 360 365	
caa ctg caa tgg ctg aac cgt cgt gct aac gct ctg ctg gct aac ggt	1152
Gln Leu Gln Trp Leu Asn Arg Ala Asn Ala Leu Leu Ala Asn Gly	
370 375 380	
gtt gaa ctg cgt gac aac cag ctg gtt gtt ccg tct gaa ggc ctg tac	1200
Val Glu Leu Arg Asp Asn Gln Leu Val Val Pro Ser Glu Gly Leu Tyr	
385 390 395 400	
ctg atc tac tcc cag gtt ctg ttc aaa ggc cag ggc tgc ccg tcc acc	1248
Leu Ile Tyr Ser Gln Val Leu Phe Lys Gly Gln Gly Cys Pro Ser Thr	
405 410 415	
cac gtt ctg ctg acc cac acc atc tct cgt atc gct gtt tcc tac cag	1296
His Val Leu Leu Thr His Thr Ile Ser Arg Ile Ala Val Ser Tyr Gln	
420 425 430	
acc aaa gta aac ctg ctg tct gca atc aaa tct ccg tgc cag cgt gaa	1344
Thr Lys Val Asn Leu Leu Ser Ala Ile Lys Ser Pro Cys Gln Arg Glu	

435

440

445

acc ccg gaa ggt gct gaa gct aaa ccg tgg tac gaa ccg atc tac ctg 1392
 Thr Pro Glu Gly Ala Glu Ala Lys Pro Trp Tyr Glu Pro Ile Tyr Leu
 450 455 460

ggt ggc gtt ttt caa ctg gag aaa ggt gac cgt ctg tct gca gaa att 1440
 Gly Gly Val Phe Gln Leu Glu Lys Gly Asp Arg Leu Ser Ala Glu Ile
 465 470 475 480

aac cgt ccg gac tac ctg gac ttc gca gaa tct ggt cag gtt tac ttc 1488
 Asn Arg Pro Asp Tyr Leu Asp Phe Ala Glu Ser Gly Gln Val Tyr Phe
 485 490 495

ggt atc atc gct ctg tga 1506
 Gly Ile Ile Ala Leu
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<210> 26

<211> 501

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: scTNF-L short chain peptide

<400> 26

Met Arg Gly Ser His His His His His His Gly Ser Ala Ser Ser Ser
 1 5 10 15

Ser Arg Thr Pro Ser Asp Lys Pro Val Ala His Val Val Ala Asn Pro
 20 25 30

Gln Ala Glu Gly Gln Leu Gln Trp Leu Asn Arg Arg Ala Asn Ala Leu
 35 40 45

Leu Ala Asn Gly Val Glu Leu Arg Asp Asn Gln Leu Val Val Pro Ser
 50 55 60

Glu Gly Leu Tyr Leu Ile Tyr Ser Gln Val Leu Phe Lys Gly Gln Gly
 65 70 75 80

Cys Pro Ser Thr His Val Leu Leu Thr His Thr Ile Ser Arg Ile Ala
 85 90 95

Val Ser Tyr Gln Thr Lys Val Asn Leu Leu Ser Ala Ile Lys Ser Pro
 100 105 110

Cys Gln Arg Glu Thr Pro Glu Gly Ala Glu Ala Lys Pro Trp Tyr Glu
115 120 125

Pro Ile Tyr Leu Gly Gly Val Phe Gln Leu Glu Lys Gly Asp Arg Leu
130 135 140

Ser Ala Glu Ile Asn Arg Pro Asp Tyr Leu Asp Phe Ala Glu Ser Gly
145 150 155 160

Gln Val Tyr Phe Gly Ile Ile Ala Leu Gly Gly Gly Ser Gly Gly Gly
165 170 175

Ser Gly Gly Gly Ser Ser Ser Arg Thr Pro Ser Asp Lys Pro Val Ala
180 185 190

His Val Val Ala Asn Pro Gln Ala Glu Gly Gln Leu Gln Trp Leu Asn
195 200 205

Arg Arg Ala Asn Ala Leu Leu Ala Asn Gly Val Glu Leu Arg Asp Asn
210 215 220

Gln Leu Val Val Pro Ser Glu Gly Leu Tyr Leu Ile Tyr Ser Gln Val
225 230 235 240

Leu Phe Lys Gly Gln Gly Cys Pro Ser Thr His Val Leu Leu Thr His
245 250 255

Thr Ile Ser Arg Ile Ala Val Ser Tyr Gln Thr Lys Val Asn Leu Leu
260 265 270

Ser Ala Ile Lys Ser Pro Cys Gln Arg Glu Thr Pro Glu Gly Ala Glu
275 280 285

Ala Lys Pro Trp Tyr Glu Pro Ile Tyr Leu Gly Gly Val Phe Gln Leu
290 295 300

Glu Lys Gly Asp Arg Leu Ser Ala Glu Ile Asn Arg Pro Asp Tyr Leu
305 310 315 320

Asp Phe Ala Glu Ser Gly Gln Val Tyr Phe Gly Ile Ile Ala Leu Gly
325 330 335

Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Ser Ser Arg Thr Pro

340

345

350

Ser Asp Lys Pro Val Ala His Val Val Ala Asn Pro Gln Ala Glu Gly
355 360 365

Gln Leu Gln Trp Leu Asn Arg Arg Ala Asn Ala Leu Leu Ala Asn Gly
370 375 380

Val Glu Leu Arg Asp Asn Gln Leu Val Val Pro Ser Glu Gly Leu Tyr
385 390 395 400

Leu Ile Tyr Ser Gln Val Leu Phe Lys Gly Gln Gly Cys Pro Ser Thr
405 410 415

His Val Leu Leu Thr His Thr Ile Ser Arg Ile Ala Val Ser Tyr Gln
420 425 430

Thr Lys Val Asn Leu Leu Ser Ala Ile Lys Ser Pro Cys Gln Arg Glu
435 440 445

Thr Pro Glu Gly Ala Glu Ala Lys Pro Trp Tyr Glu Pro Ile Tyr Leu
450 455 460

Gly Gly Val Phe Gln Leu Glu Lys